

GenCore version 5.1.3
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using SW model

SUMMARIES

Run on: February 3, 2003, 12:50:42 ; Search time 4456 Seconds
(without alignments)
16850.368 Million cell updates/sec

Title: US-10-047-593-5

Perfect score: 2580
Sequence: 1 gggcccgtaatcgtac...cgctctaggaagggtcagt 2580

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2400000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Datababe : GenEmbl:
1: gb_bp:*

2: gb_hg_g:*

3: gb_ini:*

4: gb_on:*

5: gb_ovr:*

11: gb_sc8:*

12: gb_sg:*

7: gb_pn:*

8: gb_pl:*

9: gb_pr:*

10: gb_to:*

1: em_bp:*

2: em_cro:*

27: em_gbs:*

28: em_uni:*

30: em_hg_hum:*

31: em_hg_inv:*

32: em_hg_other:*

33: em_hg_mus:*

34: em_hg_pnl:*

35: em_hg_rod:*

36: em_hg_mam:*

37: em_hg_vrt:*

38: em_hgo_hum:*

39: em_hgo_mus:*

40: em_hgo_pnl:*

41: em_hgo_other:*

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2579.6	100.0	2715	6	AX041010		AX041010 Sequence
2	2579.6	100.0	7789	6	AX041008		AX041008 Sequence
3	439	17.0	1231	8	AF050451	Zea maya	AF050451 Zea maya
4	425.6	16.5	226001	8	AF391808	Zea maya	AF391808 Zea maya
5	341.6	13.2	11587	8	AF466202	Zea maya	AF466202 Zea maya
6	331.4	12.8	7622	8	ZBMS2	Zea maya 2M	X58700 Zea maya 2M
7	328.4	12.7	95078	8	AF466931	Zea maya	AF466931 Zea maya
8	328.4	12.7	99596	8	AF466932	Zea maya	AF466932 Zea maya
9	311.4	12.1	342296	8	AF090447	Zea maya	AF090447 Zea maya
10	298.8	11.6	8227	8	AF167312	Zea maya	AF167312 Zea maya
11	295.4	11.4	130843	8	AF464738	Zea maya	AF464738 Zea maya
12	285.4	11.1	160480	8	AFL2535	Zea maya	AFL2535 Zea maya
13	285.4	11.1	1261	8	AF050452	Zea maya	AF050452 Zea maya
14	283.8	11.0	1259	8	AF050453	Zea maya	AF050453 Zea maya
15	281	10.9	3196	8	AF465642	Zea maya	AF465642 Zea maya
16	259.6	10.1	107835	8	AF078063	Zea maya	AF078063 Zea maya
17	253.2	10.0	105186	8	AF48416	Zea maya	AF48416 Zea maya
18	255.2	9.9	3892	6	AX099717	Sequence	AX099717 Sequence
19	255.6	9.8	8887	8	ZM068408	Zea maya re	U68408 Zea maya re
20	252.2	9.8	991	8	AF050450	Zea maya	AF050450 Zea maya
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22	192.6	7.5	147198	8	AF466203	Zea maya	AF466203 Zea maya
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32	100.2	3.9	9002	6	AX268055	Sequence	AX268055 Sequence
33	91.8	3.6	7218	6	166494	Sequence 14	166494 Sequence 14
34	87.6	3.4	1194	8	AF050446	Zea maya	AF050446 Zea maya
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38	76	2.9	2873	6	11774	Sequence 1	11774 Sequence 1
39	76	2.9	2873	6	I24719	Sequence 1	I24719 Sequence 1
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45	69	2.7	8039	8	AF348319	Zea maya	AF348319 Zea maya

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

TITLE	Maize npr1 polynucleotides and methods of use	Db	841	CCTTGCTTCATTTTATGTCGCTAACGGATTCTTGGTTGGTTGACCT	900
JOURNAL		Qy	901	TATGCCCTGAGATAAACACAATCTGCGCAACTAGTGATGCTCATGTTGTTGTTGAT	960
PATENT	WO 006537-A 5 02-NOV-2000;	Db	901	TATGCCCTGAGATAAACACAATCTGCGCAACTAGTGATGCTCATGTTGTTGTTGAT	960
PIONEER	INTERNATIONAL, INC. (US)	source	1.	/organism="Zea mays"	
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ORIGIN		Query	1. .2715		
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Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	Db	961	CGTCAACTAACTTATTAGAAGTGTTAACCTTATTCCCTTACAGCACT	1020
Matches 2580; Conservative 0;		Qy	1021	CTATATAGTGTGAGACCTCGACATGAAGTGTCCTAGGAAGGCCAAGGCTCTCGGTAA	1080
		Db	1021	CTATATAGTGTGAGACCTCGACATGAAGTGTCCTAGGAAGGCCAAGGCTCTCGGTAA	1080
		Qy	1081	GGTGCCTGACATCAGGACCTTAGGCCCGTTAGAATGGGCTGTCATAGAGATG	1140
		Db	1081	GGTGCCTGACATCAGGACCTTAGGCCCGTTAGAATGGGCTGTCATAGAGATG	1140
Qy	61 GAGGCCGACCGTTGCACTTGGAGCGTGGAGAATTCGATCTCTCTTATTGGC 60	Qy	1141	GGCTCTGAATGCTGAGCTCAGGACCTTAGGCCCGTTAGAATGGGCTGTCATAGAGATG	1200
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Qy	421 ACTTAGACACATACATAGCTCTAAACATGTTAAATCTGAGAACATACCTTA 480	Qy	1501	ATCAAATACCCCTTACACATTGTCCTTATTTTGTGTTCCATACAAAC	1560
Db	421 ACTTAGACACATACATAGCTCTAAACATGTTAAATCTGAGAACATACCTTA 480	Db	1501	ATCAAATACCCCTTACACATTGTCCTTATTTTGTGTTCCATACAAAC	1560
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Qy	541 ACCAAATAACTTGAATGGCCCAAGGGCACATTCCCTTCAGTCGGTSCACAC 600	Qy	1621	TAAGCTGTTGTAACAAACAACTTAATTCGAGAGGGCTTGTGATTAACTGTTCA	1680
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Qy	721 GACAGTCGATGATTAAGCGGAGCGAACATGTTGGCTGCA 780	Qy	1801	GTAGAGTTGTTACAGTTTATTAGGATTCATAGGGTTTGTGATTAACTGTTCA	1860
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Qy	781 GGGCGCGCTGGTGCACCGAACAAATCAGACACTCACT 840	Qy	1861	CATAAACTTACGCTTCTTAACTAGTACAGAAACCTTCACACCACTACTAGGA	1920
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Qy	841 CCTTGCTCTTGTGTTGACTTGTGCTGAACT 900	Qy	1921	GTACAGAAACATGGACATATGATTGAAAGAAATAATGACAGATAGGT	1980
Db	841 CCTTGCTCTTGTGTTGACTTGTGCTGAACT 900	Db	1921	GTACAGAAACATGGACATATGATTGAAAGAAATAATGACAGATAGGT	1980

DEFINITION Zea mays clone ZMMBBB_0138B04 putative aldose reductase-related protein, putative S-receptor kinase, putative genetic modifier, putative prol1, regulatory protein, putative SN protein, putative protein, putative NADP-dependent malic enzyme, putative Fourt gene/protein, and putative gag-pol precursor -orf2 genes, complete cds; and putative pol protein gene, partial cds.

ACCESSION AF466202

VERSION AF466202.1

GI:18542165

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Poales; Andropogoneae; Zea

REFERENCE 1 (bases 1 to 115787)

AUTHORS Liaca, V., Linton, E., Young, S., Kovchok, S. and Messing, J.

TITLE Direct Submission

JOURNAL Submitted (07-JAN-2002) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA

REFERENCE 2 (bases 1 to 115787)

AUTHORS Ranakrishna, W., Sam Miguel, P., Emberton, J. and Bennetzen, J.

TITLE Direct Submission

JOURNAL Submitted (07-JAN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA

FEATURES Location/Qualifiers

source

1..115787

/organism="Zea mays"

/cultivar="B'3"

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/chromosome="10"

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CDS

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CDS

mRNA

gene

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mRNA

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WFTSLAPNSTTWACLEKKFHDYFYCGETELRSLHLLTVQKNETVSEYKRFRET

TATA_signal		AF466931		LOCUS		95078 bp		DNA		1 linear		PLN 03-APR-2002	
				DEFINITION		Zea mays clone BAC 163K15, complete sequence.							
				ACCESSION		AF466931							
prim_transcript		2760..3517		VERSION		AF466931.1		G1:19908841					
		/note="P2 alternate"		KEYWORDS		/note="P2 alternate"		SOURCE		zea mays			
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Matches 454;		Conservative 0;		Mismatches 51;		Indels 42;		Gaps 5;		/note="Unpublished"		/note="Unpublished"	
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Qy		157		CACGGTGTTCGCGGGATGCCGGAGACCGTTGSCCGGACCGCTGGCTACCGG		216		/note="Unpublished"		/note="Unpublished"		/note="Unpublished"	
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REFERENCE 1 (bases 1 to 8227)
AUTHORS Christopher M.E. and Good A.G.
TITLE Evolution of a functionally related lactate dehydrogenase and
pyruvate decarboxylase pseudogene complex in maize
JOURNAL Genome 42 (6), 1167-1175 (1999)
MEDLINE 2012180
PUBMED 10659784
REFERENCE 2 (bases 1 to 8227)
AUTHORS Christopher M.E. and Good A.G.
TITLE Direct Submission
JOURNAL Submitted (08-JULY-1999) Biological Sciences, University of Alberta,
EDMONTON, AB T6G 2E9, Canada
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ACCESSION AF464738
VERSION 1.0
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REFERENCE 1 (bases 1 to 130843)
AUTHORS Linton, E., Young, S., Kovchok, S., Keizer, G., Bronzino, A., Dooley, J.
and Messing, J.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute,
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REFERENCE	AUTHORS	TITLE	JOURNAL
190	Freelinghuysen, Road, Piscataway, NJ 08854, USA		
2	Ramakrishna, W., Samiguel, P., Emberton, J. and Bennetzen, J.	Direct Submission	Submitted - DEC-2001 Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA
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RESULT	12	ACATTTCCTTCAACAGTC	590
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DEFINITION		Zea mays alcohol dehydrogenase 1 (adh1) gene, adh1-F allele, complete cds.	
ACCESSION		AF123535	
VERSION		AF123535.1	
KEYWORDS		.	
SOURCE		Zea mays.	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE		1. (bases 1 to 16480) Tikhonov,A.P., Samiguel, P.J., Nakajima, Y., Gorenstein,N.M., Bennetzen,J.L. and Avramova,Z.	
AUTHORS		Colinearity and its exceptions in orthologous adn regions of maize and sorghum Proc. Natl. Acad. Sci. U.S.A. 96 (13), 7409-7414 (1999)	
TITLE			
JOURNAL			
PUBLISHED		10377428	
REFERENCE		2 (bases 1 to 16480) Samiguel,P.J., Tikhonov,A. and Bennetzen,J.L.	
AUTHORS		Direct Submission Submitted (25-JAN-1999) Biological Sciences, Purdue University, Hansen LSRB, Rm. 339, West Lafayette, IN 47907, USA	
FEATURES		Location/Qualifiers	
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 VERSION AF050452.1 GI:3452305
 SOURCE
 ORGANISM Zea mays.
 REFERENCE Zea mays.
 AUTHORS Sam Miguel, P.J., Gaut, B.S., Tikhonov, A., Nakajima, Y. and Benetzen, J.L.
 TITLE The Paleontology of Intergene Retrotransposons of Maize: Dating the Strata
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1261)
 AUTHORS Sam Miguel, P.J.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-1998) Biological Sciences, Purdue University,
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RESULT 14
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 DEFINITION Zea mays retrotransposon Opie-3 5' LTR, partial sequence.
 ACCESSION AF050453
 VERSION AF050453.1 GI:3452306
 SOURCE
 ORGANISM Zea mays.
 REFERENCE Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 AUTHORS Sam Miguel, P.J., Gaut, B.S., Tikhonov, A., Nakajima, Y. and Benetzen, J.L.
 TITLE The Paleontology of Intergene Retrotransposons of Maize: Dating the Strata
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1259)
 AUTHORS Sam Miguel, P.J.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-1998) Biological Sciences, Purdue University,
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Qy	429 ACATACATCTAGCTTAACAAATGTTATTCCTGAGAACATACCTTATAC	488
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Qy	489 TTGACTCTGTCACC-----ATTACACTTGGACTTGTTGACACTAA	538
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Qy	539 TCACAAATACTTAAATGGCCCAAGGGCACATTCCCTCA	583
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RESULT 15		
LOCUS	AF465642	3196 bp DNA Linear PLN 03-FEB-2002
DEFINITION	Zea mays Golden cross bantam-70 lipoxygenase gene, promoter region	and Partial cds.
ACCESSION	AF465642	PACC
VERSION	AF465642.1	GI:18481646
KEYWORDS		
SOURCE		
ORGANISM	Zea mays	
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REFERENCE		
AUTHORS	Kim,E.-S. and Han,O.S.	
TITLE	Zea mays lipoxygenase promoter	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 3196)	
AUTHORS	Kim,E.-S. and Han,O.S.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-JAN-2002) Biotechnology Research Institute, Chonnam National University, 300 Yonbong-dong, Buk-gu, Kwangju 500-757, Republic of Korea	
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CDS	join(251. .2461, 2733. .3025, 3139. .>3196)	

GenCore version 5.1.3
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Om nucleic - nucleic search, using SW model

Run on:

February 3, 2003, 12:50:42 ; Search time 361 Seconds

(without alignment) 1.094.614 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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ALIGNMENTS

RESULT	ID	Description
1	ACG68802	standard; DNA; 2715 BP.
2	ACG68802	Maize NPR1 promoter
3	ACG68802;	Corn promoter clone
4	ACG68802;	Corn promoter sequ
5	ACG68802;	DNA encoding maize
6	ACG68802;	Maize glycine-rich
7	ACG68802;	Maize glycine-rich
8	ACG68802;	Maize pollen-speci
9	ACG68802;	Maize pollen-speci

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2579.6	100.0	2715 21 AAC68802	Maize NPR1 promoter
2	2579.6	100.0	7789 21 AAC68801	Maize NPR1 gene
3	256.2	9.9	3892 22 AAC6876-	Corn promoter clone
4	114.8	4.4	1587 24 AAC68666	Corn promoter sequ
5	100.2	3.9	3536 23 AAC14319	DNA encoding maize
6	100.2	3.9	8076 23 AAC14920	Maize glycine-rich
7	100.2	3.9	9002 23 AAC14921	Maize glycine-rich
8	76	2.9	2873 15 AAC54899	Maize pollen-speci
9	76	2.5	2687 15 AAC54896	Maize pollen-speci

PS Claim 13; Page 85-86; 86pp; English.

XX The present invention provides the coding and protein sequences of the
CC maize NPRI protein. NPRI controls the onset of systemic acquired
CC resistance (SAR) in plants. SAR is the mechanism by which plants acquire
CC immunity to pathogens, and the sequences provided can be used to
produce transgenic plants with increased resistance to disease.

XX SQ

Sequence 2715 BP; 645 A; 682 C; 609 G; 778 T; 1 other;
Query Match Local Similarity 100 %; Score 2579.6; DB 21; Length 2715;
Matches 2580; Conservative 100 %; Pred No. 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 GAGGCCGACCTTGGCGCTTGGACCGCTTGGCGACCCGACACTGTCCGGTGACACCG 120
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Qy 181 GCAGACCGTGGCCGGACCGACCGCTGGCTACCGAGACTGTCGGTGACACCG 240
Db 181 GCAGACCGTGGCCGGACCGACCGCTGGCTACCGAGACTGTCGGTGACACCG 240
Qy 241 CGGGGAATTAAGCGTAGCGCTAATCACTTCCGGAGGGCAAGTTCCCTGAGC 300
Db 241 CGGGGAATTAAGCGTAGCGCTAATCACTTCCGGAGGGCAAGTTCCCTGAGC 300
Qy 301 CAGGCTGGGACCGACACTGTCCGGTGACCCACGGAGCTGGTGGTGACCGCTG 360
Db 301 CAGGCTGGGACCGACACTGTCCGGTGACCCACGGAGCTGGTGGTGACCGCTG 360
Qy 361 AGCTGACTTTGGCTGACAAGTCACTTGTGACTTCACCTTGATTTCTGTGTCAGC 420
Db 361 AGCTGACTTTGGCTGACAAGTCACTTGTGACTTCACCTTGATTTCTGTGTCAGC 420
Qy 421 ACTTAGACACATACATTAGCTAAACACATGTTAACTTGAGAACATCCCTTA 480
Db 421 ACTTAGACACATACATTAGCTAAACACATGTTAACTTGAGAACATCCCTTA 480
Qy 481 TACTGGTTGACTTGTCCACCATTAAGCACTTGGCACTTGTGGACACTAATC 540
Db 481 TACTGGTTGACTTGTCCACCATTAAGCACTTGGCACTTGTGGACACTAATC 540
Qy 541 ACCAAATACTTGAATGGCCAAAGGCACATTCCCTTCAAGTCGGTGCACAC 600
Db 541 ACCAAATACTTGAATGGCCAAAGGCACATTCCCTTCAAGTCGGTGCACAC 600
Qy 601 CGGACAGTCGGCTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 660
Db 601 CGGACAGTCGGCTGACTCTGCTGCTGCTGCTGCTGCTGCTGCA 660
Qy 661 CTATAGCTTGTGACTGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCA 720
Db 661 CTATAGCTTGTGACTGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCA 720
Qy 721 GACAGTCGATGATTATAGCGGASCGGCCGCTCTGAACTTCCGGAGCTGGTGA 780
Db 721 GACAGTCGATGATTATAGCGGASCGGCCGCTCTGAACTTCCGGAGCTGGTGA 780
Qy 781 GCGGCCGCTGGCTGGCGACAGCATGTTGTCGGCCAAATCAGCACCTCAAGT 840
Db 781 GCGGCCGCTGGCTGGCGACAGCATGTTGTCGGCCAAATCAGCACCTCAAGT 840
Qy 841 CCTTGTCTTATTGTCGCTAATGATTGTTCTTGTGACCT 900
Db 841 CCTTGTCTTATTGTCGCTAATGATTGTTCTTGTGACCT 900

Qy 901 TATGACCTGAGATAATCACATCTAGCAAACTAGTAGTCCATGTTGTTGAT 960
Db 901 TATGACCTGAGATAATCACATCTAGCAAACTAGTAGTCCATGTTGTTGAT 960
Qy 961 CTCACAATCAATTAATTTATGAAAGTGGTAAACCTATATCCCTTACGACAT 1020
Db 961 CTCACAATCAATTAATTTATGAAAGTGGTAAACCTATATCCCTTACGACAT 1020
Qy 1021 CTATAGTGTGACCTGACATGAGCTGACAGCTGACAGCTGACAGCT 1080
Db 1021 CTATAGTGTGACCTGACAGCTGACAGCTGACAGCTGACAGCT 1080
Qy 1081 GGTCCTGACATGAGGACCTAGGCCCCCTAGATGGGGCTGTCATAAGAGTC 1140
Db 1081 GTCCTGACATGAGGACCTAGGCCCCCTAGATGGGGCTGTCATAAGAGTC 1140
Qy 1141 GCTCTTAAGATGATGACTGACACTGACACTGTGCTCTGCTGTTCTTAAGTATAGA 1200
Db 1141 GCTCTTAAGATGATGACTGACACTGTGCTCTGCTGTTCTTAAGTATAGA 1200
Qy 1201 TGTGTTGCCAACATCTGATGATGATGATGATGCTGTTCTTAAGTATAGA 1260
Db 1201 TGTGTTGCCAACATCTGATGATGATGATGCTGTTCTTAAGTATAGA 1260
Qy 1261 CTTTCGCTTAAAGATCCATATACATTATATTACTGTCATATATACCTCA 1320
Db 1261 CTTTCGCTTAAAGATCCATATACATTATATTACTGTCATATATACCTCA 1320
Qy 1321 CTATCTGAAATACATCTCTGGCGAAGGATAAGTGGTGGTGGAGTAAGCTGA 1380
Db 1321 CTATCTGAAATACATCTCTGGCGAAGGATAAGTGGTGGTGGAGTAAGCTGA 1380
Qy 1381 GGCACATGTGGTGCACAAACAAACATGGGGCACACACACCTCACCTATAACTA 1440
Db 1381 GGCACATGTGGTGCACAAACAAACATGGGGCACACACACCTCACCTCACCTATAACTA 1440
Qy 1441 ATTTGGCTGCAATGAGACTCCCTACGAAAGACTCTGGTGACTCTGACCAAATA 1500
Db 1441 ATTTGGCTGCAATGAGACTCCCTACGAAAGACTCTGGTGACTCTGACCAAATA 1500
Qy 1501 ATCAAATACACCTCTACGAAATGCTGCTTATTTTCTTCCATACAAAC 1560
Db 1501 ATCAAATACACCTCTACGAAATGCTGCTTATTTTCTTCCATACAAAC 1560
Qy 1561 TCAAGTGTGACTTGTGCTTACACATTGTCCTTTATTTTCTTCCATACAAAC 1620
Db 1561 TCAAGTGTGACTTGTGCTTACACATTGTCCTTTATTTTCTTCCATACAAAC 1620
Qy 1621 TAAGCTGTTGAAACACAACTAATTCGAGAGGGCTTGTGAACTGCTTAAAGTAGATTCATT 1680
Db 1621 TAAGCTGTTGAAACACAACTAATTCGAGAGGGCTTGTGAACTGCTTAAAGTAGATTCATT 1680
Qy 1681 GTGATGATTCTGGCAAGAAATCTGTTGACCTTGTGAACTGCTTAAAGTAGATTCATT 1740
Db 1681 GTGATGATTCTGGCAAGAAATCTGTTGACCTTGTGAACTGCTTAAAGTAGATTCATT 1740
Qy 1741 TTACACCTGCTGAACTGCTTGTGAACTGCTTAAAGTAGATTCATT 1800
Db 1741 TTACACCTGCTGAACTGCTTGTGAACTGCTTAAAGTAGATTCATT 1800
Qy 1801 GTAGAGTTGTGACAGTTTACCGATTCAGGTTTATAGGGATAGTGTGA 1860
Db 1801 GTAGAGTTGTGACAGTTTACCGATTCAGGTTTATAGGGATAGTGTGA 1860
Qy 1861 CATAACTCTGCTTCTTTTAACTGACAGAAACCTTACACACTCTAGGA 1920
Db 1861 CATAACTCTGCTTCTTTTAACTGACAGAAACCTTACACACTCTAGGA 1920
Qy 1921 GTCACAGAAACATGGACAAATGATTTGAAAGAAATATGACAGAAAGTGTGAACCT 1980
Db 1921 GTCACAGAAACATGGACAAATGATTTGAAAGAAATATGACAGAAAGTGTGAACCT 1980

QY	901	TATGCCACTGAGATAAATCACACTAGCCAACTAGTTAGTCATGGGTTGTGTGAT	960
Db	901	TATGCCACTGAGATAAATCACACTAGCCAACTAGTTAGTCATGGGTTGTGTGAT	960
QY	961	CCTCAACTACTAAATCTTATAGAGAAGTGTAACTTACCCATTCTCAGGACACT	1020
Db	961	CCTCAACTACTAAATCTTATAGAGAAGTGTAACTTACCCATTCTCAGGACACT	1020
QY	1021	CTATAGTGCTGAGACCTCGACATGAGAGTGTCTAGAGCAGACTCTCAGGACACT	1080
Db	1021	CTATAGTGCTGAGACCTCGACATGAGAGTGTCTAGAGCAGACTCTCAGGACACT	1080
QY	1081	GCTCTCTGACATGCAGGACCTAGGGCCGTTAGAATGGGCTTGCCATAGAGTG	1140
Db	1081	GCTCTCTGACATGCAGGACCTAGGGCCGTTAGAATGGGCTTGCCATAGAGTG	1140
QY	1141	GGCTCTAAGATCATGACTGAGACTGAGACTGTGGCTGIGCTTAAGTATAGTA	1200
Db	1141	GGCTCTAAGATCATGACTGAGACTGAGACTGTGGCTGIGCTTAAGTATAGTA	1200
QY	1201	TGTTTGCCAACATCTGATGATGATGTTGCTAACAAAGCCCTGTTTAAAGTATAGTA	1260
Db	1201	TGTTTGCCAACATCTGATGATGATGTTGCTAACAAAGCCCTGTTTAAAGTATAGTA	1260
QY	1261	CTTCCTGCTTAATAGATCCATTACATTTATTTCTATGCTATATACCTA	1320
Db	1261	CTTCCTGCTTAATAGATCCATTACATTTATTTCTATGCTATATACCTA	1320
QY	1321	CTATCTGAGAGATACATCTGTTGGAAAGATAAGTAGTGTGTTGGAGGAAGTTAGA	1380
Db	1321	CTATCTGAGAGATACATCTGTTGGAAAGATAAGTAGTGTGTTGGAGGAAGTTAGA	1380
QY	1381	GCGACANGTGGTGCACAAACAACATGGGGCACACACACCTACCTACATAACTA	1440
Db	1381	GCGACANGTGGTGCACAAACAACATGGGGCACACACACCTACCTACATAACTA	1440
QY	1441	ATTTGGCTTGCACATGGGGCACACACACCTACCTACCTACATAACTA	1500
Db	1441	ATTTGGCTTGCACATGGGGCACACACACCTACCTACCTACATAACTA	1500
QY	1501	ATCAAATACCTCTAACACATTCTCATTTATTTCTGTTCCATACAAAC	1560
Db	1501	ATCAAATACCTCTAACACATTCTCATTTATTTCTGTTCCATACAAAC	1560
QY	1561	TCAAGTGCATGTTTTGACCTTGTGACATAGCCTTAAGTAGATTCAATT	1620
Db	1561	TCAAGTGCATGTTTTGACCTTGTGACATAGCCTTAAGTAGATTCAATT	1620
QY	1621	TAAGCTGTGTTGAAACAACTAATTCTGAGAGGCTGATTGAGGACAAAGCTGG	1680
Db	1621	TAAGCTGTGTTGAAACAACTAATTCTGAGAGGCTGATTGAGGACAAAGCTGG	1680
QY	1681	GTGATGATCAATTGGACGAATCGATGTTAACCTGCTGTTGATTAATTCTAG	1740
Db	1681	GTGATGATCAATTGGACGAATCGATGTTAACCTGCTGTTGATTAATTCTAG	1740
QY	1741	TTCACACGGTGTGACACGGCGTAGGAAGTGTGTTAACCTCTTCTATATTAGA	1800
Db	1741	TTCACACGGTGTGACACGGCGTAGGAAGTGTGTTAACCTCTTCTATATTAGA	1800
QY	1801	GTAGAGTTGTACAGTTATTACGGATACGGTAACTGCTGTGATTAATTCTAG	1860
Db	1801	GTAGAGTTGTACAGTTATTACGGATACGGTAACTGCTGTGATTAATTCTAG	1860
QY	1861	CATAACTCTGACTTCTTTATAGTCACAGAACCTCACACCTACTAGA	1920
Db	1861	CATAACTCTGACTTCTTTATAGTCACAGAACCTCACACCTACTAGA	1920
QY	1921	GTAACAGAAACATGGACCATTTGAAAGAAATATGACGATAAGGT	1980
Db	1921	GTAACAGAAACATGGACCATTTGAAAGAAATATGACGATAAGGT	1980
RESULT 3			
AAF81476	ID	AAB81476 standard; DNA; 3892 BP.	XX
	AC	AAF81476;	XX
	DT	08-JUN-2001 (first entry)	XX
	DE	Corn promoter clone #700342976.	XX
	KW	Corn; promoter; transgenic plant; herbicide resistance; ds.	XX
	OS	Zea mays.	XX
	PN	WO200119976-A2.	XX
	PD	22-MAR-2001.	XX
	PP	13-SEP-2000; 2000WO-US25078.	XX
	PR	16-SEP-1999; 99US-0154182.	XX
	PA	(MONS) MONSANTO CO.	XX
	PI	Anderson HM, Chay CA, Chen G, Conner TW;	XX
	DR	WPI; 2001-244796/25.	XX
Novel promoter nucleic acid sequences useful for regulating heterologous gene expression in plants, comprising regulatory sequences located upstream to plant DNA structural coding sequences -			

XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
XX
SQ Sequence 3892 BP; 909 A; 1007 C; 877 G; 1099 T; 0 other;
Query Match 9.9%; Score 256.2; DB 22; Length 3892;
Best Local Similarity 71.3%; Pred. No. 6.3e-62;
Matches 464; Conservative 0; Mismatches 98; Indels 89; Gaps 6;
Db 20 CACTATAGGGCGAGAAATTCTGCGATCTCTCTTATTGSGAACCGACCGTGGCGCT 79
QY 2088 CACCATACACTGCGGTGCTGTTATCTGCGCACCGACCGTGGAGAT 2147
QY 80 TTTGGAGCGTGGCGACCCGACATCTCGTGGCACACCGAGCTAGTGCCCCCT 139
Db 2148 TTTGGAGCGTGGCGACCCGACATCTCGTGGCACACCGAGCTAGTGCCCCCT 2207
QY 140 CGGACCCCTGGGCCACGGTGTTCGGGGATGGCGCGCACCGTGGCGAC 199
Db 2208 CAGACCGTGGCTGGCTACCGTCAAGCGGATGGCGGCCACCGTGGCGAC 2267
QY 200 GACCGTGGCTACCGACAGTCCGGTGA-CACCGAGCTGGCGATTAATAGCCGT 258
Db 2268 GACCGTGGCTACCGACAGTCCGGTGA-CACCGAGCTGGCGATTAATAGCCGT 2327
QY 259 ACCGCGTTAACCTACTTCCGAGAGCGAGCTGGCGGCCACCGTGGCGAC 199
Db 2328 ACACCGITGATGACTTCCGAGAGCGAGCTGGCGGCCACCGTGGCGAC 295
QY 296 -----
Db 2388 GGTGATTATAGCCATAACGCCGCGAGCTGTCGGTCTAGAGGGATGTTACCGAGCTGGT 2447
QY 304 CCTGGCCACCGGAACTGTCGGTCAACCCGAGCAGTCCGGTGCACCGAG 363
Db 2448 CCTGGCCACCGGAACTGTCGGTGCACCGAG 2507
QY 364 TGACTTGGCTGAAAGCTGTTAGTCCACTGATTTCTCTGTTCCAGCT 423
Db 2508 CTACTTGGTGAACACAGCAACTCTTTCCTAATGTTCTCTGTTCTGACT 2567
QY 424 TAGACACAATACATAGCTCAAACATGTTATTCTGAGAACATACCTTATAC 483
Db 2568 TAGACACAATACATAGCTCAAACATGTTACATGTTCTGACT 2625
QY 484 TTGGTTGACTTGTCCACCA-----TTAACACTTGGCACTTGTTGGCA 533
Db 2626 TTGATTCGACTTCATCCACCATTTGGCACTTGTTAACATTTGTTGG-CA 2684
QY 534 CTAATCACCMAAATACTTAGAAATGGCCCAAGGSCACATTCCCTTCAA 584
Db 2685 CTTATATCACCMAAATACTTAGAAATGGCCCAAGGSCACATTCCCTTCAA 2735
RESULT 4
ID AAS95566
ID AAS95566 standard; DNA; 1587 BP.
XX
AC
XX
DT 26-FEB-2002 (first entry)
DE Corn promoter sequence #9.

XX
PS
XX
CC
CC
CC
CC
CC
CC
XX
SQ Sequence 1587 BP; 435 A; 385 C; 375 G; 392 T; 0 other;
Query Match 4.4%; Score 114.8; DB 24; Length 1587;
Best Local Similarity 76.9%; Pred. No. 7.8e-22; Matches 140; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Db 424 GATCTCCCTCCATATCGGGCACTGGCACCTTGCGCTTGGACCGTGGCGACCG 100
QY 41 GATCTCCCTCCATATCGGGCACTGGCACCTTGCGCTTGGACCGTGGCGACCG 483
Db 424 GATCTCCCTCCATATCGGGCACTGGCACCTTGCGCTTGGACCGTGGCGACCG 483
QY 101 ACTACTGCGGTCACCCGGACAGTCAGGTCGGCCCTTCGACCGTGGCGACCG 160
Db 484 ACTATGCGGTCACCCGGACAGTCAGGTCGGCCACACCGTGGCGACCG 543
QY 161 TGTTCGGCGATGGCGAGAGCTGGCGACCCGACCGTGGCGACCG 220
Db 544 TGTTCGGCGATGGCGAGAGCTGGCGACCCGACCGTGGCGACCG 603
QY 221 TC 222
Db 604 TC 605
RESULT 5
ID AAS14919
ID AAS14919 standard; DNA; 3536 BP.
XX

AC	AAS14919;	XX	
DT	27-FEB-2002 (first entry)	XX	
DNA	encoding maize glycine-rich promoter, ZmGRP.	XX	
XX	Maize; glycine-rich promoter; ZmGRP; transgenic plant; rye; rice; barley; sorghum; millet; sugar cane; tobacco; potato; soybean; insect resistance; herbicide resistance; stress resistance; mycotoxin; male sterility; ds.	KW	
XX	Zea mays.	OS	
PN	WO200170778-A2.	XX	
PD	27-SEP-2001.	XX	
PF	20-MAR-2001; 2001WO-US08965.	XX	
PR	21-MAR-2000; 2000US-0532806.	XX	
PA	(DEKA-) DEKALB GENETICS CORP.	XX	
PI	McElroy D, Orozco EM, Laccetti LB;	XX	
DR	WPI; 2001-626124/72.	XX	
PT	An isolated nucleic acid comprising a maize Glycine Rich Protein promoter, useful for genetically engineering commercially important plants, e.g. maize, tomato and soybean -	PT	
PR	Claim 2; Fig 4; 185pp; English.	PS	
CC	The invention relates to an isolated nucleic acid (I) comprising a maize Glycine Rich Protein (GRP) promoter, (I) may be used in the production of transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice, oat, barley, turf grass, sorghum, millet and/or sugar cane) or dicotyledonous plants (tobacco, tomato, potato, soybean (preferred), cotton, canola, alfalfa, sunflower and/or cotton) with altered properties such as insect/bacteria/fungi/virus/nematode/herbicide resistance, enhanced grain composition or quality/nutrient utilisation/environment of stress resistance, reduced mycotoxin contamination, male sterility, a selectable marker phenotype, a screenable marker phenotype, negative selectable marker phenotype or altered plant agronomic characteristics. The maize Glycine Rich Protein (GRP) promoter is a novel tool for the creation of transgenic plants (especially maize) with beneficial characteristics. The promoter minimises yield drag and other potential adverse physiological effects on maize growth and development that may be encountered by high-level, non-inducible, constitutive expression of a transgenic protein in a plant. A wider range of genetic promoters also makes it possible to introduce multiple transgenes into a plant, each of which is fused to a different promoter, therefore minimising the risk of DNA sequence homology dependent transgene inactivation (co-suppression). The present sequence represents the coding sequence of maize glycine rich promoter, ZmGRP as described in the invention.	CC	
CC	Sequence 3536 BP; 955 A; 790 C; 928 T; 0 other;	SQ	
CC	Query Match Best Local Similarity 3.9%; Score 100.2; DB 23; Length 3536; Matches 199; Conservative 63.6%; Pred. No. 1.8e-17; Mismatches 109; Indels 4; Gaps 3;	CC	
CC	Example 2; Page 176-179; 185pp; English.	CC	
CC	The invention relates to an isolated nucleic acid (I) comprising a maize Glycine Rich Protein (GRP) promoter, (I) may be used in the production of transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice, oat, barley, turf grass, sorghum, millet and/or sugar cane) or dicotyledonous plants (tobacco, tomato, potato, soybean (preferred), cotton, canola, alfalfa, sunflower and/or cotton) with altered properties such as insect/bacteria/fungi/virus/nematode/herbicide resistance, enhanced grain composition or quality/nutrient utilisation/environment of stress resistance, reduced mycotoxin contamination, male sterility, a selectable marker phenotype, a screenable marker phenotype, negative selectable marker phenotype or altered plant agronomic characteristics. The maize Glycine Rich Protein (GRP) promoter is a novel tool for the creation of transgenic plants (especially maize) with beneficial characteristics. The promoter minimises yield drag and other potential adverse physiological effects on maize growth and development that may be encountered by high-level, non-inducible, constitutive expression of a transgenic protein in a plant. A wider range of genetic promoters also makes it possible to introduce multiple transgenes into a plant, each of which is fused to a different promoter, therefore minimising the risk of DNA sequence	CC	
OY	886 GTTGTTGTGAACCTTGACCTGAGATAATCACATCTGG-CCAACTAGTGTGCCA 944	Db	1614 AGAGTGTCTTGGTCCTTCCTGCTCATTTCCTTAACCTAACTGATTTATG 1555
OY	1554 GTTGTTGTGAACCTTGACCTGAGATAATCACATCTGG-CCAACTAGTGTGCCA 1495	Db	1494 ATTTATGGTGGACATTCACCACAAATTATTATAGGAAGGTTAACCTATT 1435
OY	945 TGTTGGTGTGTTGAGCTCAACTAACTATATAGAAGTGGTAAACCTATT 1004	Db	1005 TCCTTTCAGAC 1017
OY	1434 TCCCTTCAGTC 1442	Db	
RESULT 6		Os	
AAS14920/c		Synthetic.	
ID AAS14920 standard; DNA; 8076 BP.		XX	
AC AAS14920;		XX	
XX	27-FEB-2002 (first entry)	XX	
XX	Maize glycine-rich promoter, plasmid pZmGRP-GN73.	DR	
XX	Maize; glycine-rich promoter; ZmGRP; transgenic plant; rye; rice; barley; sorghum; millet; sugar cane; tobacco; potato; soybean; insect resistance; herbicide resistance; stress resistance; mycotoxin; male sterility; plasmid; pZmGRP-GN73; circular; ds.	XX	
XX	Zea mays.	OS	
XX	W0200170778-A2.	XX	
XX	27-SEP-2001.	XX	
XX	20-MAR-2001; 2001WO-US08965.	XX	
XX	21-MAR-2000; 2000US-0532806.	XX	
XX	(DEKA-) DEKALB GENETICS CORP.	PA	
XX	McElroy D, Orozco EM, Laccetti LB;	PI	
XX	WPI; 2001-626124/72.	DR	
XX	An isolated nucleic acid comprising a maize Glycine Rich Protein promoter, useful for genetically engineering commercially important plants, e.g. maize, tomato and soybean -	PT	
XX	Example 2; Page 176-179; 185pp; English.	PS	
XX	The invention relates to an isolated nucleic acid (I) comprising a maize Glycine Rich Protein (GRP) promoter, (I) may be used in the production of transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice, oat, barley, turf grass, sorghum, millet and/or sugar cane) or dicotyledonous plants (tobacco, tomato, potato, soybean (preferred), cotton, canola, alfalfa, sunflower and/or cotton) with altered properties such as insect/bacteria/fungi/virus/nematode/herbicide resistance, enhanced grain composition or quality/nutrient utilisation/environment of stress resistance, reduced mycotoxin contamination, male sterility, a selectable marker phenotype, a screenable marker phenotype, negative selectable marker phenotype or altered plant agronomic characteristics. The maize Glycine Rich Protein (GRP) promoter is a novel tool for the creation of transgenic plants (especially maize) with beneficial characteristics. The promoter minimises yield drag and other potential adverse physiological effects on maize growth and development that may be encountered by high-level, non-inducible, constitutive expression of a transgenic protein in a plant. A wider range of genetic promoters also makes it possible to introduce multiple transgenes into a plant, each of which is fused to a different promoter, therefore minimising the risk of DNA sequence	CC	
OY	706 TCGCTGCTGTCGATGATGTTAGCGGACGGCCCTGGCTGGTGCACCAA 765	Db	1671 GGTTAGA-GTTCGCATATGTCGGCTGGACGACA-GTCGGTGGCCAGACC 1615
OY	1731 TCCGTGGCACACTGGACATTCCGGTGAATTAGCGGAGCCGGCTCAGAACCAA 1672	Db	826 TCAGCACACTCAAGTCCTGCTCATTTATGTCGTAACGGATTCTTGT 885

CC homology dependent transgene inactivation (co-suppression). The
 CC present sequence represents the coding sequence of maize glycine-rich
 CC promoter, plasmid pZMGRP-GN73 as described in the invention.
 XX Sequence 8076 BP; 2129 A; 1960 C; 1952 G; 2035 T; 0 other;
 SQ Query Match 3.9%; Score 100.2; DB 23; Length 8076;
 Best Local Similarity 63.6%; Pred. No. 2; 9e-17; Mismatches 109; Indels 1; Gaps 3;
 Matches 199; Conservative 1; Mismatches 109; Indels 4; Gaps 3;
 OY 706 TCCGGCTGCTGACATCGGAACTTATAGGGASCGGCCCTGAAATCCGAG 765
 Db 1744 TCCGGCTGCTGACATCGGAACTTATAGGGASCGGCCCTGAAATCCGAG 1685
 Db 1684 GTTAAGA-GTTGCATATGTAGCGCCTGGGCAACGACA 825
 OY 826 TAGCACACTGAGCTTGCTTCACTTATGCTTATTCACCTAATGTTATGG 885
 Db 1627 AGAGTACTCTGGTTCTTGTGATCTTACCTAATGTTATGG 1568
 OY 886 GTTGTGTTGACCTATGACCTTAGATAATCATCATCTAG-CCAAATGAGTCA 944
 Db 1567 GTTGTGTTGACCTTAGACCTTAGAGCTTAGATATAATCTAGAGAACATTAGTCCA 1508
 OY 945 TCTGGTTGTTGACCTTAGACCTTAGAGCTTAGATATAATCTAGAGAACATTAGTCCA 1004
 Db 1507 ATTATTTGTTGACCTTAGACCTAACCAACCAAAATTATTTAGGAAGGTAAACCTATT 1448
 OY 1005 TCCCTTCAGCAC 1017
 Db 1447 TCCCTTCAGCTC 1435

RESULT 7
 AAS14921 standard; DNA; 9002 BP.
 AC AAS14921;
 XX DT 27-FEB-2002 (first entry)
 DE Maize glycine-rich promoter, Plasmid pZMGRP-Act2-int-GN73.
 XX KW Maize; glycine-rich promoter; Zmgrp; transgenic plant; rye; rice;
 KW barley; sorghum; millet; sugar cane; tobacco; potato; soybean;
 KW insect resistance; herbicide resistance; stress resistance; mycotoxin;
 KW male sterility; plasmid; pZMGRP-Act2-int-GN73; circular; ds;
 OS Zea mays.
 OS Oryza sativa.
 OS Synthetic.
 PN WO200170778-A2.
 XX PD 27-SEP-2001.
 XX PF 20-MAR-2001; 2001WO-US08965.
 PR 21-MAR-2000; 2000US-0532806.
 PA (DEKA-) DEKALB GENETICS CORP.
 XX PI McElroy D, Orozco EM, Laccetti LB;
 XX DR WPI; 2001-626124-/72.

XX An isolated nucleic acid comprising a maize Glycine Rich Protein
 PT promoter, useful for genetically engineering commercially important
 PT plants, e.g. maize, tomato and soybean -
 XX Example 2; Page 179-182; 185pp; English.

XX The invention relates to an isolated nucleic acid (1) comprising a maize
 CC Glycine Rich Protein (GRP) promoter. (1) may be used in the production of
 CC transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice,
 CC oat, barley, turf grass, sorghum, millet and/or sugar cane) or
 CC dicotyledonous plant (tobacco, tomato, potato, soybean (preferred),
 CC cotton, canola, alfalfa, sunflower and/or cotton) with altered
 CC properties such as insect/bacteria/fungi/viral/nematode/herbicide
 CC resistance, enhanced grain composition or quality/nutrient
 CC utilisation/environment or stress resistance, reduced mycotoxin
 CC contamination, male sterility, a selectable marker phenotype, a
 CC screenable marker phenotype, negative selectable marker phenotype, a
 CC or altered plant agronomic characteristics. The maize Glycine Rich
 CC Protein (GRP) promoter is a novel tool for the creation of transgenic
 CC plants (especially maize) with beneficial characteristics. The promoter
 minimises yield drag and other potential adverse physiological effects
 CC on maize growth and development that may be encountered by high-level,
 CC non-inducible, constitutive expression of a transgenic protein in a
 plant. A wider range of genetic promoters also makes it possible to
 introduce multiple transgenes into a plant, each of which is fused to a
 different promoter, therefore minimising the risk of DNA sequence
 homology dependent transgene inactivation (co-suppression). The
 present sequence represents the coding sequence of maize glycine-rich
 CC promoter, plasmid pZMGRP-Act2-int-GN73 containing the rice Act2-
 CC intron deletion derivative, Act2-int, as described in the invention.
 XX Sequence 9002 BP; 2342 A; 2123 C; 2136 G; 2351 T; 50 other;
 SQ Query Match 3.9%; Score 100.2; DB 23; Length 9002;
 Best Local Similarity 63.6%; Pred. No. 3; 1e-17; Mismatches 109; Indels 1; Gaps 3;
 Matches 199; Conservative 1; Mismatches 109; Indels 4; Gaps 3;
 OY 706 TCCGGCTGCTGACATCGGAACTTATAGGGASCGGCCCTGAAATCCGAG 765
 Db 1747 TCCGGCTGCTGACATCGGAACTTATAGGGASCGGCCCTGAAATCCGAG 1688
 OY 766 TCCGGCTGCTGACATCGGAACTTATAGGGASCGGCCCTGAAATCCGAG 765
 Db 1687 GTTAAGA-GTTGCATATGTAGCGCCTGGGCAACGACA 825
 OY 826 TAGCACACTGAGCTTGCTTCACTTATGCTTATTCACCTAATGTTATGG 885
 Db 1630 AGAGTACTCTGGTTCTTGTGCTTATTCACCTAATGTTATGG 1571
 OY 886 GTTGTGTTGACCTATGACCTTAGATAATCATCATCTAG-CCAAATGAGTCA 944
 Db 1570 GTTGTGTTGACCTTAGACCTTAGAGCTAGATATAATCTAGAGAACATTAGTCCA 1511
 OY 945 TCTGGTTGTTGACCTTAGACCTTAGAGCTAGATATAATCTAGAGAACATTAGTCCA 1004
 Db 1510 ATTATTTGTTGACCTTAGACCTAACCAACCAAAATTATTTAGGAAGGTAAACCTATT 1451
 OY 1005 TCCCTTCAGCAC 1017
 Db 1450 TCCCTTCAGCTC 1438

RESULT 8
 AAQ54889 standard; DNA; 2873 BP.
 XX ID AAQ54889
 XX AC AAQ54889;
 XX DT 26-JAN-1995 (first entry)
 DE Maize pollen-specific polygalacturonase gene upstream sequence.
 XX KW Maize; pollen specific expression; polygalacturonase gene; promoter;
 XX inbred corn variety W22; chimeric gene; ds.
 OS Zea mays.
 XX Key Location/Qualifiers

CC MAR2 and MAR3 were cloned to construct plasmids pZ01927, pZ01929
 CC and pSVB20-SAR (L) for gene activity.
 XX Sequence 862 BP; 259 A; 176 C; 178 G; 249 T; 0 other;
 SQ Best Local Similarity 2.1%; Score 53; DB 15; Length 862;
 Matches 121; Conservative 0; Mismatches 75; Indels 3; Gaps 2;

QY	840	TCTTCTTCCTCTTATGTCGCTACTGGATTCTTGTGTTGTTGTTGACCG 899
	855	TCTGTGCGAAATAATCAGCTTCTGGATAGATAGTGTTGTTGTTGTTGAC 796
QY	900	TTATGCCACTGAGATAATCACATCTGCAACTAGTAGTCTGTTGTTGTTGAC 959
	795	TTATGCACCTG-GAATGATCACTAGACAAACTGCTTGTGTTGTTGTTGAC 737
Db	960	TCTGCAACTACTAAATCTATTTAGAAGTGTGTTAACCTTACACAC 1019
	736	TCTCAACACCCAAATGATPATAGGAAT-GTTCAGACTATTCCCTCACACTA 679
QY	1020	TCTATATGTCGTGAGAC 1038
Db	678	CATATAGTTGCAAC 660

RESULT 11

ID	AA235393_c	standard; DNA; 23449 BP.
XX	AA235393;	
AC		
XX	DT	27-MAR-2000 (first entry)
DE	Maize amylose-extender (Ae) gene encoding starch branching enzyme.	
XX	KW	Starch branching enzyme Iib; amylose-extender gene; Ae gene; maize; corn; promoter; expression control element; endosperm; transgenic plant; ss.
XX	OS	zea mays.
XX	Key	Location/Qualifiers
FH	misc_signal	597..602
FT		/tag= a
FT		/note= "I box, conserved in RBCS genes"
FT	repeat_unit	1475..1481
FT		/tag= b
FT	misc_signal	/note= "RY repeat, distal regulatory element" 1967..1973
FT		/tag= c
FT	misc_signal	/note= "hex, conserved element found in plant histone gene promoters"
FT	misc_signal	2593..2599
FT		/tag= d
FT		/note= "MRE box, motif essential for metal ion-dependent induction of metallothionein genes"
FT	GC_signal	2666..2671
FT		/tag= e
FT	GC_signal	2738..2743
FT		/tag= f
FT	GC_signal	2831..2836
FT		/tag= g
FT	misc_signal	2838..2844
FT		/tag= h
FT		/note= "MRE box, motif essential for metal ion-dependent induction of metallothionein genes"
FT	GC_signal	2874..2879
FT		/tag= i
FT	TATA_signal	2933..2936
FT		/tag= j

FT CDS 3065..19659
 FT /tag= k
 FT /note= "contains introns"
 FT 2965..3176
 FT /tag= l
 FT /note= 1
 FT /tag= m
 FT /note= 1
 FT /tag= n
 FT /note= 1
 FT /tag= o
 FT /note= 2
 FT /tag= p
 FT /note= 3
 FT /tag= q
 FT /note= 3
 FT /tag= r
 FT /note= 4
 FT /tag= s
 FT /note= 4
 FT /tag= t
 FT /note= 5
 FT /tag= u
 FT /note= 5
 FT /tag= v
 FT /note= 6
 FT /tag= w
 FT /note= 6
 FT /tag= x
 FT /note= 7
 FT /tag= y
 FT /note= 7
 FT /tag= z
 FT /note= 8
 FT /tag= aa
 FT /note= 8
 FT /tag= ab
 FT /note= 9
 FT /tag= ac
 FT /note= 9
 FT /tag= ad
 FT /note= 10
 FT /tag= ae
 FT /note= 10
 FT /tag= ah
 FT /note= 11
 FT /tag= ag
 FT /note= 11
 FT /tag= ah
 FT /note= 12
 FT /tag= j
 FT /note= 12
 FT /tag= j

FT (UYPE-) UNIV PENNSYLVANIA STATE.
 FT XX
 FT Guiltinan MJ, Kim K;
 FT XX
 FT WPI; 2000-116538/10.
 FT DR
 FT XX
 FT PT New gene regulatory sequences from plants used to provide resistance to
 FT microbial path pathogens -
 FT XX
 FT Query Match 2.0%; Score 52.8; DB 21; length 23449;
 FT Matches 179; Conservatve 1; Mismatches 13; Indels 17; Gap 3;
 FT Best Local Similarity 54.2%; Pred. No. 0.018; DB 21; length 23449;
 FT QY 717 ACCGAGACGTCCATGAAATTATAGCGGAGCGGCCTTGAACTTCCCGAGTGGCCCTGTT 776
 FT DB 23383 ACCGGAGACTCCCGTGAAATTAGCGGAGCGCCTTGAAAGGGGGAGGAGTT 23324
 FT QY 777 TGAGGGGCCATGGCTGGTGACCGAACATGATGGCCCAAATCAGCACACTC 836
 FT DB 23323 CASCCTGTGAG-TCCCCTGTGACCGAACACTGG-----CHACACTCG 23280
 FT QY 837 AGTCCTTGTCTCATTTTATGTCGCTAACAGATTCTTTGGTTGTGTTGA 896
 FT DB 23279 TATCCCTTGTCTTTTGTGACCTAGTTCTGCTTATTGGCTAAGTGAA 23220
 FT QY 897 ACCTTATGCACTGTGAGATAAACATCTAGCCAACCTAGTAGTCATGTTGCT 956
 FT DB 23219 CCTTGGACCTGTATACTTATACACTAGAGCCAACTAGTTAGTCCTTAATTGTGTT 23160
 FT QY 957 TGTTCG-TCAACTACTAAACTATTATAGAAAGCTGTTAACCTTATTCCCTTCAGC 1015
 FT DB 23159 GAGAAATTGACACCAAAATCAATTAGGAACTAGTGTAAGCTATTCCCTTCATC 23100
 FT QY 1016 ACTCTCTATGTCGTGAGCTGACA 1045
 FT DB 23099 TCCCCCTTGTGATGCGAACACA 23070
 FT RESULT 12
 FT AAH88703
 FT ID AAH88703 standard; DNA; 123219 BP.
 FT XX
 FT AAH88703;
 FT XX
 FT DT 26-FEB-2002 (first entry)
 FT DE Human DNA sequence SEQ ID 543.
 FT XX
 FT KW Single nucleotide polymorphism; SNP; biallelic marker; human;
 FT KW central nervous system disorder; CNS; db.
 FT OS Homo sapiens.
 FT XX
 FT PN W020151659-A2.
 FT XX
 FT PD 19-JUL-2001.
 FT XX
 FT PP 11-JAN-2001; 2001WO-1B00116.
 FT XX
 FT PR 13-JAN-2000; 2000US-0175854.
 FT XX
 FT PA (GEST) GENSET.
 FT XX
 FT PI Chu T, Blumenfeld M, Cohen D;
 FT XX
 FT DR
 FT XX
 FT PT Isolated polymucleotides, useful for genotyping nucleic acids for
 FT PT biallelic markers for the diagnosis of depression, comprises central
 FT PT nervous system disorder related biallelic marker -
 FT XX
 PS Disclosure; Page 439-472; 519pp; English.

XX 11-JUN-1999; 99MO-US13266.
 XX 12-JUN-1998; 98US-0089049.
 PR 12-JUN-1998; 98US-0089050.

XX WO9964562-A2.
 PD 16-DEC-1999.
 XX
 XX
 PN
 PR
 XX

XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation
 XX Claim 1; SEQ ID NO 1163; 32BP + Sequence listing; German.
 XX The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, leukaemia, Alzheimer's disease, AIDS,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX Sequence 6215 BP; 1586 A; 169 C; 1366 G; 3094 T; 0 other;
 SQ Query Match 1.8%; Score 47.6; DB 24; Length 6215;
 Best Local Similarity 47.6%; Pred. No. 0.025; Mismatches 189; Indels 6; Gaps 1;
 Matches 177; Conservative 0; PT
 QY 1524 TTGTGCCATTATATTTCGTTCCATACAACTCAAGTACTGTTTGTGA 1583
 Db 3889 TTATATGATTTTTTGTAGATAATTATTTTTATTTTGAT 3948
 QY 1584 CCTTGACACAGACCTTAAGTAGATTCAATTAACTGTTATGAAACAAAC 1643
 Db 3949 TATTATTTTTTTTTTAAATTAAATTAAATTAAAGTTGTGTTTGTGATT 4008
 QY 1644 TATTGAGAGAGCGTGTAGGAGAACCTGGCGTCAATGTCATTGAGCAA 1703
 Db 4009 TTGTGTTAGTTGAGATAATTAAATGATGGATGTTTGTGATTGATT 4068
 QY 1704 TCGATGTTAACGTCGCTGTGATTAATTCTACCTTCACACGGTGAACCGCGTA 1763
 Db 4069 TATAGAGGTGATTAAATTAAATTAAATTAAATTAAATTAAATTAAAGTGAAGG 4128
 QY 1764 GGAGTGT-----TGAATTCCCTCTTGTGATTATAGAGTAGAGTTGTACAG 1817
 Db 4129 AGAAAATGTTAAATTAAATGATGATGTTGTGAAAGATGTTGGAGTGTAGA 4188
 QY 1818 TTATTTAGGTTTACCGTAAATTAGGGTTAGGTGACTGACTAACTTGCTT 1877
 Db 4189 TTGTGTTAGTTTATGAAATTGTGAGATTGTGAGATGAGATGGTTTT 4248
 QY 1878 TCTTTTAATA 1889
 Db 4249 TATTATTTATA 4260

XX Sequence 5572 BP; 1307 A; 195 C; 1274 G; 2796 T; 0 other;
 SQ Query Match 1.8%; Score 47.4; DB 24; Length 5572;
 Best Local Similarity 46.3%; Pred. No. 0.027; Mismatches 181; Indels 0; Gaps 0;
 Matches 156; Conservative 0; PT
 QY 1561 TCAAGTGTACTGTTTGACCTTGACCATAGCCTTAAGTAGATTCAATT 1620
 Db 4630 TAGATGGTTGAAATTTCAGTTAGTTAATTAGTTCTTGTGTTTAANGT 4689
 QY 1621 TAAGCTGTATGTAACAAACAACTAATTTCGAGAGGCTGTGTTGAGGAGAAGTCGCG 1680
 Db 4690 TGGATATAGGGTGTGACTTATGTTGGTTAATTGGATGTTAGGTTCGTT 4749
 QY 1681 GTGGATGATGTCATTGGCGAATCGATGTTAACCTGCTGTGATTAATTCTAG 1740
 Db 4750 GTTGTGGTTATTGGGATTAGTTAATTGTGAGATTATTGTGAGTTTGTAGA 4809
 QY 1741 TCCACAGGTGTGTCAGGGCTAGGAAGTGTGGAATTCCCTCTATGATTAATA 1800
 Db 4810 TTTTGTGTTGAAATGTTATTTTTTTTTTTTTTTTTTTTGAGTGTAGA 4869
 QY 1801 GTRGAGTTGTACGTTATTAGGATTCATTACGGTTATTAGGGATACGTGA 1860
 Db 4870 GATATTGTAGTATTTGAGATGATGTTAGGATTTAGGATTTAGTATATGG 4929
 QY 1861 CTATAACTGAGCTCTTTTATAGTCACAG 1897
 Db 4930 AAATGTTAAATTATTTATTTGATTA 4966

RESULT 15
 ABL54360 PR 06-APR-2000; 2000DE-1019058.
 ID PR 07-APR-2000; 2000DE-1019173.
 XX PR 30-JUN-2000; 2000DE-1032529.
 AC PR 01-SEP-2000; 2000DE-1043826.
 ABL54360; PA (EPIC-) BIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2002-017444/02.
 XX PT Chemically modified sequences of genes associated with apoptosis are
 CC useful to determine methylation patterns of genomic DNA samples for
 CC diagnosis of associated diseases such as cancer.
 XX PS Claim 1; Seq ID #60; 24PP; English.
 XX This invention relates to chemically pre-treated DNA of genes
 CC associated with apoptosis. The nucleic acids are used to allocate
 patients for specific therapy for HIV infection, Bloom syndrome,
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus
 CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours
 CC and cancers. This nucleotide sequence represents a chemically
 treated apoptosis gene. Even SEQ ID numbers are the complementary
 DNA strands to the odd SEQ ID numbers. The sequence data for this
 CC patent is not represented in the printed specification but is based on
 information supplied by the European patent office.
 XX Sequence 5572 BP; 1307 A; 195 C; 1274 G; 2796 T; 0 other;
 SQ Query Match 1.8%; Score 47.4; DB 24; Length 5572;
 Best Local Similarity 46.3%; Pred. No. 0.027; Mismatches 181; Indels 0; Gaps 0;
 Matches 156; Conservative 0; PT
 QY 1561 TCAAGTGTACTGTTTGACCTTGACCATAGCCTTAAGTAGATTCAATT 1620
 Db 4630 TAGATGGTTGAAATTTCAGTTAGTTAATTAGTTCTTGTGTTTAANGT 4689
 QY 1621 TAAGCTGTATGTAACAAACAACTAATTTCGAGAGGCTGTGTTGAGGAGAAGTCGCG 1680
 Db 4690 TGGATATAGGGTGTGACTTATGTTGGTTAATTGGATGTTAGGTTCGTT 4749
 QY 1681 GTGGATGATGTCATTGGCGAATCGATGTTAACCTGCTGTGATTAATTCTAG 1740
 Db 4750 GTTGTGGTTATTGGGATTAGTTAATTGTGAGATTATTGTGAGTTTGTAGA 4809
 QY 1741 TCCACAGGTGTGTCAGGGCTAGGAAGTGTGGAATTCCCTCTATGATTAATA 1800
 Db 4810 TTTTGTGTTGAAATGTTATTTTTTTTTTTTTTTTTTGAGTGTAGA 4869
 QY 1801 GTRGAGTTGTACGTTATTAGGATTCATTACGGTTATTAGGGATACGTGA 1860
 Db 4870 GATATTGTAGTATTTGAGATGATGTTAGGATTTAGGATTTAGTATATGG 4929
 QY 1861 CTATAACTGAGCTCTTTTATAGTCACAG 1897
 Db 4930 AAATGTTAAATTATTTATTTGATTA 4966

Search completed: February 3, 2003, 16:20:48
 Job time : 727 secS

XX Apoptosis; HIV; Bloom syndrome; cardiopathy;
 KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
 KW amyotrophic lateral sclerosis; cancer; db.
 OS Unidentified.
 XX PN WO200177164-A2.
 XX PD 18-OCT-2001.
 XX PP 06-APR-2001; 2001WO-EP03969.

